

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2002, 02:35:48 ; Search time 1906.95 seconds
(without alignments)
24766.091 Million cell updates/sec

Title: US-09-652-292-1
Perfect score: 4395
Sequence: 1 gagggggccctgcagggcc.....attattttgaaaaaaaaaaaaa 4395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vit:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	738.4	16.8	910	10	AL554162
2	669	15.2	859	11	BG563879
3	636.4	14.5	685	11	BG568246
4	627.4	14.3	678	13	AQ037826
5	606.8	13.8	706	11	BG566556
6	590.4	13.4	925	11	BG569139
7	576.4	13.1	580	10	AA628914
8	574.6	13.1	1049	11	BF688799
9	548.2	12.5	563	10	AI042706
10	526.4	12.0	528	10	AA404352
11	525.6	12.0	532	10	AI041537
12	492.4	11.2	523	10	AW298226

13	485.2	11.0	624	11	W02942
14	478	10.9	479	10	AL449907
15	471.2	10.7	481	10	AL449906
16	466	10.6	466	10	AL449914
17	460	10.5	461	10	AL449913
18	457.4	10.4	459	10	AL449887
19	455.6	10.4	482	10	AW973035
20	454.6	10.3	511	11	N36110
21	454	10.3	454	10	AI334230
22	448.6	10.2	475	10	AL449910
23	448.6	10.2	495	10	AA007343
24	443.6	10.1	561	10	AA133966
25	443.4	10.1	467	10	AA403072
26	437.4	10.0	453	10	AA133497
27	429.8	9.8	450	10	AI081145
28	427.4	9.7	450	10	AL449886
29	424.2	9.7	454	10	AI753293
30	423.4	9.6	485	11	W39026
31	419.4	9.5	440	10	AI082631
32	417.4	9.5	431	10	AI097288
33	415.8	9.5	425	10	AA134031
34	408.4	9.3	456	10	AA115737
35	405	9.2	540	10	BE237601
36	400.6	9.1	479	10	AA007344
37	397	9.0	429	10	AA232787
38	393.6	9.0	634	10	AL576963
39	386.4	8.8	430	10	AL449909
40	386.4	8.8	432	10	AL449908
41	386	8.8	415	10	AI292321
42	384.6	8.8	411	11	N93207
43	379	8.6	402	10	AL449905
44	377.8	8.6	405	10	AI753932
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ALIGNMENTS

RESULT 1	AL554162	910 bp	mRNA	EST	16-FEB-2001
LOCUS	AL554162	LTI_NFL005_PL2	Homo sapiens	cDNA clone	CS0DI081YA24 5
DEFINITION	prime, mRNA sequence.				
ACCESSION	AL554162				
VERSION	AL554162.1	GI:12894675			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 910)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
FEATURES	Location/Qualifiers				
source	1..910				
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	/db_xref="taxon:9606"				
	/clone="CS0DI081YA24"				
	/clone_lib="LTI_NFL005_PL2"				
	/issue_type="placenta"				
	/notes="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371				

W02942	za06g06.r1
AL449907	AL449907
AL449906	AL449906
AL449914	AL449914
AL449913	AL449913
AL449887	AL449887
AW973035	EST395132
N36110	YY32f01.s1
AI334230	qq09h04.x
AL449910	AL449910
AA007343	zh97f12.r
AA133966	z134g09.s
AA403072	zv63f10.r
AA133497	z896b03.f
AI081145	oz66g03.x
AL449886	AL449886
AI753293	cf08b03.x
W39026	zb34h02.r1
AI082631	ox58h07.s
AI097288	qb88j01.x
AA134031	z134g09.f
AA115737	zk96b03.s
BE237601	146953.MA
AA007344	zb97f12.s
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AL449909	AL449909
AL449908	AL449908
AI292321	qm77a08.x
N93207	zb27h12.s1
AL449905	AL449905
AI753932	cf16c08.x
AL449904	AL449904

Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT	115 a	282 C	264 g	222 t	27 others
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Query Match	16.8%	Score 738.4	DB 10	Length 910	
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				Indels	15
				Gaps	10
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Qy	239	tccgcctcgccatgggcacatcccaactctccctctctctctctctctctctctctctctc	298		
Db	61	tccgcgcgcgcacatgggcacastctcactctgctctctctctctctctctctctctctctc	120		
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Db	121	tggcgtgtggcctgacctttgcttatgaactggcagtcataatcagtgccctgctgcac	180		
Qy	356	tgaacttgac-tttgggctaagctgttgagcaggagt--cctggcggcagcctgc	412		
Db	181	tgcagcttgacttttggcctgawctkvttttwtwtatcttcttkttkkcgacgctgc	240		
Qy	413	tcttggggg-----ctc	468		
Db	241	tcttggggggtc	300		
Qy	469	aggaaagaagcactctctgggagcaacttgctgctggcagcagcctgacccggc	528		
Db	301	aggaaagaagcactctctgggagcacttgctgctggcagcagcctgacccggc	360		
Qy	529	ctgactgttccctggcctgagctgctggcgcgcgcctgctggttggtctctctctctctc	588		
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Db	421	ctctctctctctggtctgtctatctcagagctggcggcagcagcgaggga	480		
Qy	649	gtcctgtgtctctctctatgaagcagcagcagcagcagcagcagcagcagcagcagc	708		
Db	481	gtcctgtgtctctctctatgaagcagcagcagcagcagcagcagcagcagcagcagc	540		
Qy	709	aactatgactggcctgtgtacccctgggagtgaggagcagctgtcggcctggcagcagc	768		
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Qy	829	acacagaagacatcactcactcagggagctgagcccccagcagcagcagcagcagcag	888		
Db	660	acacagaagacatcactcactcagggagctgagcccccagcagcagcagcagcagcag	719		
Qy	889	ccaggtactctcttctggaactctcagggcagcagcagcagcagcagcagcagcagc	948		
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Qy	949	gtgggctggggtcgggt--gtctctccagcagcagcagcagcagcagcagcagcagc	1007		
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Qy	1008	tgcctccacatctcagcctcgtgtgttctcaggggagcctcagcagcagcagcagc	1067		
Db	840	tgcctccacatctcagcctcgtgtgttctcaggggagcctcagcagcagcagcagc	898		
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Db	899	tgtggggctggg 910			


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sequence.
ACCESSION AQ037826
VERSION AQ037826.1 GI:3303658
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
            Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
            Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
            Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other-GSSs: CIT-HSP-2326p11.TR
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.

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BASE COUNT	204 a	124 c	120 g	230 t	
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Query Match	14.3%	Score 627.4;	DB 13;	Length 678;	
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Matches 628;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
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Db	50	CAAGCTGTGAGAGCTGGTGTGCTACATTTTCAGGATTTTACAAGTTGGTAAACACAGCC	109		
QY	3442	attataaaaaattaaatgatttaaaattataaataagtaaatcacattaaacaaaaaaa	3501		
Db	110	ATTATATAAAATTTAAATGATTTAAATTTATAATTAAGTAAATACATTAACAAAAA	169		
QY	3502	ttatactcaaaattcattacttaatttttactactggttactattatactgtgcgtttgagg	3561		
Db	170	TTATACTCAAAATTCATTACTTAATTTTACTACTCTGTACTATTATCTGTGCTTTTGAGG	229		
QY	3562	ctattttcacatagtaactctttatgagacctatgaggacctaggagacacgcgcactctcttcctga	3621		
Db	230	CTATTTCATACATAGTAACTCCTTATGGAGACCTAGGGGAGACACCGCGCATCTCTTCCTGA	289		
QY	3622	ttcccaactcaatgacatactatgtagtctttgttggtccttaactcggctcgtgggagtgctt	3681		
Db	290	TTCCCCACTCAATGACATCATGTTAGTCTTTGGTTGGTTAACTGGCTGTGGGGAGTGCTTT	349		
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QY	3742	tctagacttcagaacatgctcgggataaaatgcagtaatgcagatttaaacctttaaagtatg	3801		

D	B	410	TC	TAGACTTCGAGAACAATGCCTGGATAAAATGTCAAGTAATGAACATTTAAAGTATG	469		
Q	Y	3802	tctt	gtttgtagccaatacatcagtggtatagacacaaaaaatggaggattattcttcacg	3861		
D	B	470	TC	TGTTGTGAGCCAATACATCGTGTTATAGCACCAAAAAATGGAGGATTATTCTCCAG	529		
Q	Y	3862	tagt	gaacaactgtctaccgcttticagctgcacagtgcgtaaacattcatttaagaaggagttc	3921		
D	B	530	TAG	TTGAACACTGCTCATCCGCTTTTCAGCTGCAGCTGCTCAAATCATTTAAGAAGGAGTTC	589		
Q	Y	3922	tgac	attcatttcatttgttttaccttttcttctccactagtgtaaacacaaaatttcaa	3981		
D	B	590	TGAC	ATTCATTTTTATTGTTTTTACTTTTGTTCTCCTCAGTAGTAAACAAAATTTCAA	649		
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LOCUS		BG566556	706 bp	mRNA	EST 10-APR-2001		
DEFINITION		602585538F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4714365 5', mRNA sequence.					
ACCESSION		BG566556					
VERSION		BG566556.1	GI:13574209				
KEYWORDS		EST.					
SOURCE		human.					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE		1 (bases 1 to 706)					
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.					
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgab@remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI559 row: e column: 22 High quality sequence stop: 649. Location/Qualifiers I. 706 .organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4714365" /clone_lib="NIH_MGC_76" /lab_host="DHIOB (T1 phage-resistant)" /notes="Organ: liver; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggccattatgcc); Site:2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCGACATG-df(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library." BASE COUNT 179 a 161 c 173 g 193 t ORIGIN					
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RESULT 6
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LOCUS 602588391F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4722431 5',
DEFINITION mRNA sequence.
ACCESSION BC569139
VERSION BC569139.1 GI:13576792
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CMI580 row: e column: 24
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High quality sequence stop: 640.
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pDMR-LIB (Clontech); Site_1:
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3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 263 a 257 c 149 g 256 t
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Query Match 13.4%; Score 590.4; DB 11; Length 925;
Best Local Similarity 93.9%; Pred. No. 3.2e-79;
Matches 723; Conservative 0; Mismatches 36; Indels 11; Gaps 10;
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QY 3872 ctgtcaccctgttcagctgcacagctgctcaaatcaatttaagaagaggtctctcagacattcat 3931
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QY 3932 ttctcattgttttactttt-gtcttcctcactagtgtaaac-aaaaatttcaaccagacatt 3989
Db 539 TTTTCATTGTTTTTACTTTTTTCTGCTTCTCTCTAGTAGTGTAAACAAAAAAATTTTCAACAGCATTT 598
QY 3990 catgccaactataccccattcttcagtcagctagctagctacagt-tatcaggagatt-ttta 4047
Db 599 CATGCCGAACCTATACCATTTCTTCACTGCTAGCTAGCTGTACAGTCTATACAGGATTTCTTCA 658
QY 4048 ttcgtagctcaattttt-gtcaaatcatgcccacaaatc-gcagtgat-agttgacttttggg 4103
Db 659 TAGGTAGTCTTAACCTCTCGTCCACATCATGCGGCCATGTAAGTCGACTCGACTCCGCA 718
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Qy 4104 tacaaggtttggcaaaaaaaattatacaaaaaattcttctgttaagaatc 4153
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Db 719 TACAAGGCTTGGCACAAGCAGCCTTACCCAAACTATCCGCCGCCGAACC 768

RESULT 7
AA628914/c
LOCUS
af28a03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1032940 3', mRNA sequence.
ACCESSION
AA628914
VERSION
AA628914.1 GI:2541301
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 580)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 481.
FEATURES
source
1..580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1032940"
/lab_host="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand
cDNA was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCACTCAGAGTGGAGCGCGCTTAATTTTCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Ronaldo."
BASE COUNT 197 a 104 c 90 g 189 t
ORIGIN

Query Match 13.1%; Score 576.4; DB 10; Length 580;
Best Local Similarity 99.8%; Pred. No. 4.5e-77;
Matches 577; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3637 catcatgttagcttctggttaactggtgctgtgggagtggtttgtatcacaaagat 3696
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 580 CATCATGTTAGTCTTTGGTTCCTAACTGGCTGTGGGAGTGTTTGTATCAACAAGAT 521

Qy 3697 tagagaggactacacatcaggcgctgatttattgttggattttctagactcagaac 3756
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 TAGAGAGGACTACATCAGGCGTCTGATTATTTGTTGTTGTTCTAGACTTCAGAAC 461

Qy 3757 atcctggataaaatgcagtaataatgaacttaagaatgtctgtttgttagcca 3816
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 ATGCTGGATAAATGTCAGTAATGCAATTAACCTTTAAAGTATGTCCTGTTTGTAGCCA 401

Qy 3817 atacatgtgtatagcaccacaaaaatggaggattattcttccctagtgtaaacactgc 3876
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 ATACATGTTGTATAGCACCACAAAATGGAGGATTATCTTCCAGTAGTGAACACTGTC 341

Qy 3877 atcgtttcagctgacagctgctcaaatcatcttaagaaggagttctgacattcttca 3936
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 ATCGTTTTCAGCTGACAGCTGCTCAAAATCATTTAAGAAGGAGTCTTGACATTTTCA 281

Qy 3937 ttgtttacatttcttctcactagtgtaacacaaaaatttcaaacagcattcatgcgc 3996
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Db 280 TTGTTTACTTTTTTCTCTCTCTCACTAGTGTAAACAAAAATTTCAACGAGCATTCATCCG 221

Qy 3997 aacctataccattcttcaagtgcttagctgtacagttatcagggttttttattctgtagtc 4056
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 220 AACCTATACCCATCTTCAGTGCCTAGCTGTACAGTATTATCAGGGATTTTATTCTGCTAGTC 161

Qy 4057 taatttgcataatcatgcccacaaatcgcagtgatagtttgatcttggatatacaaggctttggc 4116
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Db 160 TAATTTTGTCAAAATCATGCGCAAAATCGCAGTGATAGTTGACTTTTGGATACAAAGGTTTGGC 101

Qy 4117 aaaaaaaattatacaaaaattcttctglaagaatcaattggctatatatggaatttagga 4176
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Db 100 AAAAAAAATATTAACAAAATATTCTGAAGAATCAATTTGGCTATATGGAATTAGGA 41

Qy 4177 taaagaattattacaataaagaattattacaataaaga 4214
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Db 40 TAAAGAATATTACAAATAAAGAAATATTACATAAANA 3

RESULT 8
BF688799 1049 bp mRNA EST 22-DEC-2000
LOCUS
602184982F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299237 5',
DEFINITION
mRNA sequence.
ACCESSION
BF688799
VERSION
BF688799.1 GI:11974207
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1049)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1156 row: d column: 22
High quality sequence stop: 635.
FEATURES
source
1..1049
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4299237"
/tissue_type="NIH_MGC_43"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 231 a, 331 c 229 g 258 t

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QY 4116 caaaaaaaattattacaaaattctgtgaagaatcaattggctatatggatttagg 4175
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 Db 263 CAAAAAATAATTAACAATAATCTCTAAGAATCAATTGCTATATGGAATTTAGG 204
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 QY 4176 ataagaattattacaataagaattattacaataagaattattattatttgaatt 4235
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 Db 203 ATAAGAATAATTACAAATAAAGAATAATTACAAATAAAGAAGTTTATTATTATTGTAAGTT 144
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 QY 4236 gtgtgcaaaaacataccctttatctgtctgtataatttatcacacaaaattacaagaag 4295
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 Db 143 GTGTGCACAAACATACCCCTTATCTCTGTAAATTTATACACACAAAATTAACAAAAG 84
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 QY 4296 attctgtlaagaattattggctatatggatttaggataagaattattacaataagaagta 4355
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 Db 83 ATTCTGTGAAGAATAATTGGCTATATGGAATTTAGGATAGATAATTATACATAAAGAGTA 24
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 QY 4356 tttaacaataaaga 4368
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 Db 23 TTTTACATAAATA 11
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RESULT 10
 AA04352/c
 LOCUS
 DEFINITION
 zvg3f10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
 IMAGE:758347 3', mRNA sequence.
 ACCESSION
 AA04352
 VERSION
 AA04352.1 GI:2059077
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 528)
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
 Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
 ,T., Waterston,R. and Wilson,R.
 WashU-Merck EST Project 1997
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -4iml3 fwd. ET from Amersham
 High quality sequence stop: 464.
 Location/Qualifiers
 1..528
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 /db_xref="taxon:9606"
 /clone_image="758347"
 /clone_lib="Soares_total_fetus_Nb2HF8_9w"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer [5'
 TTTTACCAATCTGAAGTGGAGCGGCTTAATTTTATTTTATTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

181 a 77 c 75 g 195 t

BASE COUNT
 ORIGIN

Query Match 12.0%; Score 526.4; DB 10; Length 528;
 Best Local Similarity 99.8%; Pred. No. 1.4e-69;
 Matches 527; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3865 ttgaacactgtcatccgtttcagctgacagctgctcaaatcaattgaagaggattctga 3924
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 Db 528 TTGAACACTGTCATCCGTTTCAGCTGACAGCTGCTCAATCATTTAAGAAGGAGTTCTGA 469
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 QY 3925 cattcatctcatgttttactttgtcttccactagtgtaacaaaaattttcaacca 3984
 |||||
 Db 468 CATTCAATTTCAATGTTTACTTTGTCTTCCCTACCTAGTGTAAACAAAATTTTCAACCA 409
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 QY 3985 gcattcatgcgcgaacctatataccattcttcagtcctagctgacagttatcaggagatt 4044
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 Db 408 GCATTCAATGCGGAACCTATATACCCATTCTTCAGTGCCTAGCTGTACACTTATCAGGAGATT 349
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 QY 4045 ttattcgtagctcaatttttgcataatcatgcccataatcgccagtgatagttgactttgat 4104
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 Db 348 TTATTTCGTAGTCTAAATTTTGTCAAAATCATGCGCAAAATCGCAGTGCATAGTTGACTTTGGAT 289
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 QY 4105 acaaggtttggcaaaaaataatttaacaaaattattcgaataattctgtaagaatcaattggctata 4164
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 Db 288 ACAAGGTTTGGCAAAAAAATAATTAAACAAATATCTGTAAAGATCAATTGCGCTATA 229
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 QY 4165 tggcaattgaagataagaatatttacaataaagaatatttacaataaagaattattattattatt 4224
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 Db 228 TGGCAATTTAGGATAAACAATATTTACAATAAAGAATATTTACAATAAAGAGTTTATTATT 169
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 QY 4225 atttgtaagtgtgtgcacacacacataccctttatctctgtataaattttatcacacacaaaa 4284
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 Db 168 ATTTGTAAGTTGTGAGCAACAACATACCCCTTTATCTCTGTAAATTTTATACACACAAAA 109
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 QY 4285 attcaaaaaagattctgtgaagaattattgctatattggaatttaggataagaattattac 4344
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 Db 108 ATTAACAAAAGATCTGTAAAGATTAATTGGCTATATGGAATTTAGGATGAATATTATTAC 49
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 QY 4345 aataaagagatttacaataaagaattgtttgtattattttgtataaataaaaaa 4392
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 Db 48 AATAAAGAGTATTACAATAAAGAGTTTGTATTATTATTGTGTAATAAAAAA 1

RESULT 11
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 DEFINITION
 ov82b10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643803
 3', mRNA sequence.
 ACCESSION
 A1041537
 VERSION
 A1041537.1 GI:3280731
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 532)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/obrp/image/image.html
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 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 444.
 Location/Qualifiers
 1..532
 /organism="Homo sapiens"

CONTACT	COMMENT
<p>Contact: Stavrides GS The Sanger Centre Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK Email: humquerry@sanger.ac.uk Sanger Centre name : sccd3097.</p>	

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FEATURES
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BASE COUNT      137 a      126 c      109 g      107 t

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QY 2705	ttggctctgcttggtgtcattgctgttagaataagccacagggcctcagtttcccccatttgtat	2764		
Db				
478	TTGGTCTGCTGGTGTCTATGCTGTAGGAATAACACACGGCGCTCAGTTTCCCATTTGCTAT	419		
QY 2765	aattgggaagcctgtaccaggtcattcttaagatttctctgaactccagtcagctgggaatt	2824		
Db				
418	AATGGGAAGCCCTGTACCAGAGTCATCTTAAAGTTTCCTGACTCCAGTGCAGCTGGGAATT	359		
QY 2825	ctaaatgctggtctaggagctgtctccaggaatggtgcaggatggctttgcggaagaagaga	2884		
Db				
358	CTAATGCTGGCTAGGAGCTGTCTCCAGGATGGTGCAAGATGGCTTTCGCGAAGGAGA	299		
QY 2885	tgggttttggaggccaaacaaacctgcttgbtcaatatattgccttttgccctcttggcagcccttg	2944		
Db				
298	TGGTTTTGGAGGCCAACAAACCTGCTTGTCAATATTGGCTTTGGCTCTCTTGCAGCGCCCTG	239		
QY 2945	aacttgagtataataacaaacctcctgaacctcagttctctcatctgcagaataatggggataat	3004		
Db				
238	AACTTGAGTAAATAACAACCTCCCTGAACTCAGTTTCTCTATCTGCAGAAATGGGGATAAT	179		
QY 3005	tatgtccacaggggtatatttagaaccttgcttccctttcagagaggtcccccagctgggtccag	3064		
Db				
178	TATGTCCACAGGGGTATATTTTAGACCCCTGTTTTCCTTTTACAGGAGGTGCCACAGCTGGTCCAG	119		
QY 3065	ggccttgggaattctacttattctctcattaccacaggtctccttccctttggacccctgtaaaagg	3124		
Db				
118	GGCCTGGGAATTTCTACTTATCTCATTTACCCAGGTCCCTCCTTTGGACCCCTGTAAAGG	59		
QY 3125	gtcaggggtgaatcagatagggggactgacgaagtgcgtctatgactgcagatcatgtaagg	3182		
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58	GTCAGGGTGAATCAGATCGGGGACTGACGAAGTAGCTATGACTGCAGATCATGTGAAGG	1		

RESULT	15	
AL449906		
LOCUS		
DEFINITION		15-NOV-2000
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ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
		human.
		AL449906.1 GI:11181531
		EST.
		AL449906 Homo sapiens
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		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE		
AUTHORS		1 (bases 1 to 481)
TITLE		Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL		Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
COMMENT		Unpublished (2000)
		Contact: Stavrides GS

FEATURES

The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humqueresanger.ac.uk
Sanger Centre name : scc03096.
Location/Qualifiers

FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/map="20"
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	/tissue_type="lung"
	/dev_stage="fetal"
	/note="cDNA fragment isolated using a cDNA end rescue technique"
BASE COUNT	114 a 114 c 124 g 127 t 2 others

BASE COUNT	114 a	114 c	124 g	127 t	2 others
ORIGIN	technique 114 a 114 c 124 g 127 t 2 others				
Query Match	10.7%; Score 471.2; DB 10; Length 483;				
Best Local Similarity	99.4%; Pred. No. 2.8e-51;				
Matches 473; Conservative	0; Mismatches 3; Indels 0; Gaps				
Qy 2729	aggaatgccacagggcctcagtttccccatttgtataaagggaagcctgtaccaggtcat 2781				
Db 1	AGGAATGCCACAGGGCCCTCAGTTTCCCATTTGTATAAATGGGAAGCCTGTACCAGGTCAAT 60				
Qy 2789	tcctaaagatttcctgaactccagtcagctggaattctataaactcgtcgttagagagctgc 2841				
Db 61	TCCTTAAGATTTTCTCTGACTCCAGTCGAGCTGGGAATTTCTAAATCTCTGCTTAGGAGCTGTC 120				
Qy 2849	tccaggaaggtgcaggaatgcctttgcggaagagagatgggttttggagggccacacaaacctg 2901				
Db 121	TCCAGGATGGTGCAGGATGGCTTTGGGAAAGGAGATGGGTTTTGGAGGGCCACAAACCTG 180				
Qy 2909	ctttcctaattgaccttgcctttgcctcttggcagaccttgaaacttgagtaaaatacaaacctccct 2961				
Db 181	CTTGTGCAATATTGCCTTTGGCTCTTGGCAGCCCTTGAACCTTGAGTAAATAACAACCTCCCT 240				
Qy 2969	gaacctcagtttccctcatctgcagaatggggaacaattatgtcccaggggtatatattagac 3021				
Db 241	GAACCTCAGTTTCCCTCATCTGCAGATGGGGATAAATATGTCCACAGGGGTATATTTTAGAC 300				
Qy 3029	cctgttttccttcaaggagggtccccagctagctccagggcctcagggaattctctacttatcc 3081				
Db 301	CCTGTTTTCTTTTCAGGAGGTCCTCCACGCTGGTCAGGGCCTGGGAAATTTCTACTTATCC 360				
Qy 3089	tcattaccaggctccctccctttggaccctgaagggtcaggtgaatcagatggggggac 3141				
Db 361	TCATTACCAGGTCCTTCTCTTTGGACCTCTGAANGGTCAGGGTGAATCAGATGGGGGAC 420				
Qy 3149	tggcaggtgactatgactgcagatcatgttaagggaaggagctgacaaagactccc 3204				
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Job time: 5906 sec

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